



PATENT

Client-Matter No.: 66661-024
(P-IS 4534)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:)	Confirmation No.:	3321
Aebersold and Goodlett)		
)	Group Art Unit:	1639
Serial No.: 09/748,793)		
)	Examiner:	M. Tran
Filed: December 26, 2000)		
)		
For: METHODS FOR RAPID AND)		
QUANTITATIVE PROTEOME)		
ANALYSIS)		
)		

JUN 30 2004

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

TECH CENTER 1600/2900

Sir:

DECLARATION PURSUANT TO 37 C.F.R. § 1.132

I, David G. Camp II, declare as follows:

1) I am a Senior Research Scientist in the department of Biological Systems Analysis and Mass Spectrometry at the Pacific Northwest National Laboratory (PNNL), Richland, Washington, and associate director for the PNNL Proteomic National Center for Research Resources.

2) I received my doctorate in chemistry from the University of Montana. I have extensive experience in the area of proteomics and analysis using mass spectrometry. A copy of my curriculum vitae is attached.

3) I have reviewed the specification, the references cited in the Office Action mailed December 19, 2003, the relevant portions of the Office Action related to the rejections over these references, and the claims as I understand they will be amended in response to the Office Action.

4) I understand that the claims stand rejected, in part, as allegedly anticipated by Masselon et al., Anal. Chem. 72:1918-1924 (2000), Yates, J. Mass Spectrom. 33:1-19 (1998), and Clauser et al., Proc. Natl. Acad. Sci. USA 92:5072-5076 (1995), and as allegedly obvious over Clauser et al. in view of Gygi et al., Nat. Biotechnol. 17:994-999 (1999).

5) With regard to Masselon et al., this reference compares peptides analyzed by mass spectrometry (MS) to a database generated by *in silico* trypsin digestion of *Caenorhabditis elegans* genomic sequence. The database used by Masselon et al. does not contain multiple characteristics for the polypeptides, in contrast to the annotated polypeptide index recited in the claims.

6) Regarding Yates, this reference, similar to Masselon et al., describes the use of a database of predicted values based on *in silico* digestion with a site specific enzyme. The database described by Yates does not contain multiple characteristics for the polypeptides, in contrast to the annotated polypeptide index recited in the claims.

7) With respect to Clauser et al., this reference describes the use of a database constructed from a theoretical digest of the OWL protein sequence database. Although Clauser et al. describes using liquid chromatography to separate peptides, this information is not used as part of the identification of the proteins. The database described by Clauser et al. does not contain multiple characteristics for the polypeptides, in contrast to the annotated polypeptide index recited in the claims.

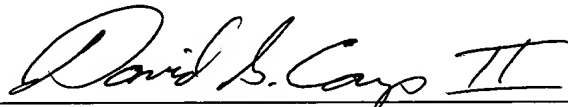
8) In conclusion, I believe that none of the references by Masselon et al., Yates or Clauser et al. describe the claimed methods using a database containing multiple characteristics of polypeptides, as in the annotated polypeptide index recited in the claims.

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that any such willful false statement may jeopardize the validity of the application or any patent issued thereon.

5.20.04

Date



Signature

David G. Camp II, Ph.D.

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel in the order listed for Form Page 2.
Follow the sample format on preceding page for each person. **DO NOT EXCEED FOUR PAGES.**

NAME		POSITION TITLE		
David G. Camp II, Ph.D.		Senior Research Scientist		
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)				
INSTITUTION AND LOCATION		DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
Albertson's College of Idaho, Caldwell, ID		B.S.	1981	Chemistry
University of Montana, Missoula, MT		Ph.D.	1988	Chemistry
University of Houston, TX		Postdoc	1988-89	
Pacific Northwest National Laboratory (PNNL), Richland, WA		Postdoc	2001-02	

Professional Experience

1981 – 1985	Graduate Teaching Assistant, University of Montana, Missoula, MT
1982 – 1988	Graduate Research Assistant, University of Montana, Missoula, MT
1988 – 1989	Postdoctoral Research Associate, University of Houston, TX
1989 – 1994	Assistant Professor of Chemistry, Eastern Oregon University, La Grande, OR
1994	Awarded Indefinite Tenure at Eastern Oregon University, La Grande, OR
1994 – 1999	Associate Professor of Chemistry, Eastern Oregon University, La Grande, OR
01/00 – 02/01	Self-employment, Boise, ID
01/01 – 02/01	Adjunct Professor of Chemistry, Boise State University, Boise, ID
2001 – 2002	Postdoctoral Research Associate, PNNL, Richland, WA
2002 – present	Senior Research Scientist, PNNL, Richland, WA
2003 – present	Associate Director for the PNNL Proteomic National Center for Research Resources

Publications

"High-throughput proteomics using Fourier transform ion cyclotron resonance mass spectrometry." Wei-Jun Qian, David G. Camp II, & Richard D. Smith, *Expert Review of Proteomics* In press (2004).

"Integrative analysis of the mitochondrial proteome in yeast." Holger Prokisch*, Curt Scharfe*, David G. Camp II*, Wenzhong Xiao*, Lior David, Christophe Andreoli, Matthew E. Monroe, Ronald J. Moore, Marina A. Gritsenko, Christian Kozany, Kim K. Hixson, Heather M. Mottaz, Hans Zischka, Marius Ueffing, Zelek S. Herman, Ronald W. Davis, Thomas Meitinger, Peter J. Oefner, Richard D. Smith, & Lars M. Steinmetz (*These authors contributed equally to this work.), *PLoS Biology* In press (2004).

"Global analysis of the membrane subproteome of *Pseudomonas aeruginosa* using liquid chromatography-tandem mass spectrometry." J. Blonder, M.B. Goshe, W. Xiao, D.G. Camp II, M. Wingerd, R.W. Davis, & R.D. Smith, *J. Proteome Res.* In press (2004).

"Improved detection of multi-phosphorylated peptides in the presence of phosphoric acid in liquid chromatography-mass spectrometry." J. Kim, D.G. Camp II, & R.D. Smith, *J. Mass Spectrom.* **39**, 208-215 (2004).

- “Ultra high efficiency strong cation exchange LC/RPLC/MS/MS for high dynamic range characterization of the human plasma proteome.” Y. Shen, J.M. Jacobs, D.G. Camp II, R. Fang, R.J. Moore, R.J. W. Xiao, R.W. Davis, R.G. Tompkins, & R.D. Smith, *Anal. Chem.*, 76, 1134-1144 (2004).
- “Nanoscale proteomics.” Y. Shen, N. Tolic, C. Masselon, L. Pasa-Tolic, D.G. Camp II, M.S. Lipton, G.A. Anderson, and R.D. Smith, *Anal. & Bioanal. Chem.* 378, 1037-1045 (2004).
- “Ultrasensitive proteomics using high-efficiency on-line micro-SPE-nanoLC-nanoESI MS and MS/MS.” Y. Shen, N. Tolic, C. Masselon, L. Pasa-Tolic, D.G. Camp II, K.K. Hixson, R. Zhao, G.A. Anderson, and R.D. Smith, *Anal. Chem.* 76, 144-154 (2004).
- “Multidimensional proteome analysis of human mammary epithelial cells.” J.M. Jacobs, H.M. Mottaz, L.-R. Yu, D.J. Anderson, R.J. Moore, W.U. Chen, K.J. Auberry, E.F. Strittmatter, M.E. Monroe, B.D. Thrall, D.G. Camp II, and R.D. Smith, *J. Proteome Res.*, 3, 68-75 (2004).
- “Phosphoprotein isotope-coded solid-phase tag approach for enrichment and quantitative analysis of phosphopeptides from complex mixtures.” W.-J., Qian, M.B. Gosh, D.G. Camp II, L.-R. Yu, K. Tang, & R.D. Smith, *Anal. Chem.*, 75, 5441-5450 (2003).
- “Detection of in situ labeled cell surface proteins by mass spectrometry: application to the membrane subproteome of human mammary epithelial cells,” W.U. Chen, L.-R. Yu, E.F. Strittmatter, B.D. Thrall, D.G. Camp II, and R.D. Smith, *Proteomics*, 3, 1647-1651 (2003).
- “Evaluation of enzymatic digestion and liquid chromatography-mass spectrometry peptide mapping of the integral membrane protein bacteriorhodopsin,” K.K. Hixson, N. Rodriguez, D.G. Camp II, E.F. Strittmatter, M.S. Lipton, and R.D. Smith, *Electrophoresis* 23, 3224-3232 (2002).
- “Accurate Molecular Weight Determination of Plasmid DNA Using Mass Spectrometry,” X. Cheng, D.G. Camp II, Q. Wu, R. Bakhtiar, D.L. Springer, B.J. Morris, J.E. Bruce, G.A. Anderson, C.G. Edmonds, and R.D. Smith, *Nucleic Acids Res.*, 24, 2183-2189 (1996).
- “Observation of a small oligonucleotide duplex by electrospray ionization-mass spectrometry,” K.J. Light-Wahl, D.L. Springer, B.E. Winger, C.G. Edmonds, D.G. Camp II, B.D. Thrall, and R.D. Smith, *J. Amer. Chem. Soc.*, 115, 803-804 (1993).
- “Direct observation of a DNA quadruplex by electrospray ionization mass spectrometry,” D.R. Goodlett, D.G. Camp II, C.C. Hardin, M. Corregan, and R.D. Smith, *Biol. Mass Spectrom.*, 22, 181-183 (1993).
- “Phylogenetic evidence for tertiary interactions in 16S-like ribosomal RNA,” T. Haselman, D.G. Camp, and G.E. Fox, *Nucleic Acids Res.*, 17, 2215-2221 (1989).
- “Probing ribosome structure and function using short oligonucleotides,” W.E. Hill, D.G. Camp, W.E. Tappich, and A. Tassanakajohn, *Methods in Enzymology*, 164, 401-419 (1988).